

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/511,549
Source: PC
Date Processed by STIC: 11/2/04

ENTERED

**CRF Errors Edited by the STIC Systems
Branch**

Serial Number:

10/511,549

CRF Edit Date:

11/2/04

Edited by:

TE

Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

Corrected the SEQ ID NO. Sequence numbers edited were:

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

Deleted: ☒ invalid beginning/end-of-file text ; ☐ page numbers

Inserted mandatory headings/numeric identifiers, specifically:

Moved responses to same line as heading/numeric identifier, specifically:

Other:



PCT

RAW SEQUENCE LISTING

DATE: 11/02/2004

PATENT APPLICATION: US/10/511,549

TIME: 16:26:53

Input Set : A:\pto.kd.txt

Output Set: N:\CRF4\11022004\J511549.raw

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3 <110> APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
5 <120> TITLE OF INVENTION: Screening method of agents for increasing insulin content
7 <130> FILE REFERENCE: Y0352PCT-698
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/511,549
C--> 9 <141> CURRENT FILING DATE: 2004-10-18
9 <150> PRIOR APPLICATION NUMBER: JP 2002-265622
10 <151> PRIOR FILING DATE: 2002-09-11
12 <150> PRIOR APPLICATION NUMBER: JP 2003-056813
13 <151> PRIOR FILING DATE: 2003-03-04
15 <160> NUMBER OF SEQ ID NOS: 7
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1008
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo sapiens
22 <220> FEATURE:
23 <223> OTHER INFORMATION: Inventor: Ohishi, Takahide; Koizumi, Tomonobu
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (1)..(1008)
29 <400> SEQUENCE: 1
30 atg gaa tca tct ttc tca ttt gga gtg atc ctt gct gtc ctg gcc tcc 48
31 Met Glu Ser Ser Phe Ser Phe Gly Val Ile Leu Ala Val Leu Ala Ser
32 1 5 10 15
34 ctc atc att gct act aac aca cta gtg gct gtg gct gtg ctg ctg ttg 96
35 Leu Ile Ile Ala Thr Asn Thr Leu Val Ala Val Ala Val Leu Leu Leu
36 20 25 30
38 atc cac aag aat gat ggt gtc agt ctc tgc ttc acc ttg aat ctg gct 144
39 Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu Ala
40 35 40 45
42 gtg gct gac acc ttg att ggt gtg gcc atc tct ggc cta ctc aca gac 192
43 Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr Asp
44 50 55 60
46 cag ctc tcc agc cct tct cgg ccc aca cag aag acc ctg tgc agc ctg 240
47 Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser Leu
48 65 70 75 80
50 cgg atg gca ttt gtc act tcc tcc gca gct gcc tct gtc ctc acg gtc 288
51 Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ala Ser Val Leu Thr Val
52 85 90 95
54 atg ctg atc acc ttt gac agg tac ctt gcc atc aag cag ccc ttc cgc 336
55 Met Leu Ile Thr Phe Asp Arg Tyr Leu Ala Ile Lys Gln Pro Phe Arg
56 100 105 110
58 tac ttg aag atc atg agt ggg ttc gtg gcc ggg gcc tgc att gcc ggg 384
59 Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala Gly

```

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60          115          120          125
62 ctg tgg tta gtg tct tac ctc att ggc ttc ctc cca ctc gga atc ccc 432
63 Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile Pro
64          130          135          140
66 atg ttc cag cag act gcc tac aaa ggg cag tgc agc ttc ttt gct gta 480
67 Met Phe Gln Gln Thr Ala Tyr Lys Gly Gln Cys Ser Phe Phe Ala Val
68 145          150          155          160
70 ttt cac cct cac ttc gtg ctg acc ctc tcc tgc gtt ggc ttc ttc cca 528
71 Phe His Pro His Phe Val Leu Thr Leu Ser Cys Val Gly Phe Phe Pro
72          165          170          175
74 gcc atg ctc ctc ttt gtc ttc ttc tac tgc gac atg ctc aag att gcc 576
75 Ala Met Leu Leu Phe Val Phe Phe Tyr Cys Asp Met Leu Lys Ile Ala
76          180          185          190
78 tcc atg cac agc cag cag att cga aag atg gaa cat gca gga gcc atg 624
79 Ser Met His Ser Gln Gln Ile Arg Lys Met Glu His Ala Gly Ala Met
80          195          200          205
82 gct gga ggt tat cga tcc cca cgg act ccc agc gac ttc aaa gct ctc 672
83 Ala Gly Gly Tyr Arg Ser Pro Arg Thr Pro Ser Asp Phe Lys Ala Leu
84          210          215          220
86 cgt act gtg tct gtt ctc att ggg agc ttt gct cta tcc tgg acc ccc 720
87 Arg Thr Val Ser Val Leu Ile Gly Ser Phe Ala Leu Ser Trp Thr Pro
88 225          230          235          240
90 ttc ctt atc act ggc att gtg cag gtg gcc tgc cag gag tgt cac ctc 768
91 Phe Leu Ile Thr Gly Ile Val Gln Val Ala Cys Gln Glu Cys His Leu
92          245          250          255
94 tac cta gtg ctg gaa cgg tac ctg tgg ctg ctc ggc gtg ggc aac tcc 816
95 Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu Gly Val Gly Asn Ser
96          260          265          270
98 ctg ctc aac cca ctc atc tat gcc tat tgg cag aag gag gtg cga ctg 864
99 Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln Lys Glu Val Arg Leu
100          275          280          285
102 cag ctc tac cac atg gcc cta gga gtg aag aag gtg ctc acc tca ttc 912
103 Gln Leu Tyr His Met Ala Leu Gly Val Lys Lys Val Leu Thr Ser Phe
104          290          295          300
106 ctc ctc ttt ctc tcg gcc agg aat tgt ggc cca gag agg ccc agg gaa 960
107 Leu Leu Phe Leu Ser Ala Arg Asn Cys Gly Pro Glu Arg Pro Arg Glu
108 305          310          315          320
110 agt tcc tgt cac atc gtc act atc tcc agc tca gag ttt gat ggc taa 1008
111 Ser Ser Cys His Ile Val Thr Ile Ser Ser Ser Glu Phe Asp Gly
112          325          330          335
115 <210> SEQ ID NO: 2
116 <211> LENGTH: 335
117 <212> TYPE: PRT
118 <213> ORGANISM: Homo sapiens
120 <400> SEQUENCE: 2
121 Met Glu Ser Ser Phe Ser Phe Gly Val Ile Leu Ala Val Leu Ala Ser
122 1          5          10          15
123 Leu Ile Ile Ala Thr Asn Thr Leu Val Ala Val Ala Val Leu Leu Leu
124          20          25          30

```

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125 Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu Ala
126           35                      40                      45
127 Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr Asp
128           50                      55                      60
129 Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser Leu
130 65                      70                      75                      80
131 Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ala Ser Val Leu Thr Val
132                      85                      90                      95
133 Met Leu Ile Thr Phe Asp Arg Tyr Leu Ala Ile Lys Gln Pro Phe Arg
134                      100                     105                     110
135 Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala Gly
136                      115                     120                     125
137 Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile Pro
138          130                      135                      140
139 Met Phe Gln Gln Thr Ala Tyr Lys Gly Gln Cys Ser Phe Phe Ala Val
140 145                      150                      155                      160
141 Phe His Pro His Phe Val Leu Thr Leu Ser Cys Val Gly Phe Phe Pro
142                      165                      170                      175
143 Ala Met Leu Leu Phe Val Phe Phe Tyr Cys Asp Met Leu Lys Ile Ala
144                      180                      185                      190
145 Ser Met His Ser Gln Gln Ile Arg Lys Met Glu His Ala Gly Ala Met
146          195                      200                      205
147 Ala Gly Gly Tyr Arg Ser Pro Arg Thr Pro Ser Asp Phe Lys Ala Leu
148          210                      215                      220
149 Arg Thr Val Ser Val Leu Ile Gly Ser Phe Ala Leu Ser Trp Thr Pro
150 225                      230                      235                      240
151 Phe Leu Ile Thr Gly Ile Val Gln Val Ala Cys Gln Glu Cys His Leu
152                      245                      250                      255
153 Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu Gly Val Gly Asn Ser
154          260                      265                      270
155 Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln Lys Glu Val Arg Leu
156          275                      280                      285
157 Gln Leu Tyr His Met Ala Leu Gly Val Lys Lys Val Leu Thr Ser Phe
158          290                      295                      300
159 Leu Leu Phe Leu Ser Ala Arg Asn Cys Gly Pro Glu Arg Pro Arg Glu
160 305                      310                      315                      320
161 Ser Ser Cys His Ile Val Thr Ile Ser Ser Ser Glu Phe Asp Gly
162          325                      330                      335
165 <210> SEQ ID NO: 3
166 <211> LENGTH: 1008
167 <212> TYPE: DNA
168 <213> ORGANISM: Rattus sp.
170 <220> FEATURE:
171 <221> NAME/KEY: CDS
172 <222> LOCATION: (1)..(1008)
174 <400> SEQUENCE: 3
175 atg gag tca tct ttc tca ttt gga gtg atc ctt gct gtc ctg acc atc 48
176 Met Glu Ser Ser Phe Ser Phe Gly Val Ile Leu Ala Val Leu Thr Ile
177 1                      5                      10                      15

```

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179	ctt	atc	att	gct	gtt	aat	gcg	ctg	gtg	gtt	gtg	gct	atg	ctg	cta	tca	96
180	Leu	Ile	Ile	Ala	Val	Asn	Ala	Leu	Val	Val	Val	Ala	Met	Leu	Leu	Ser	
181				20				25					30				
183	atc	tac	aag	aat	gat	ggt	gtt	ggc	ctt	tgc	ttc	acc	tta	aat	ctg	gcc	144
184	Ile	Tyr	Lys	Asn	Asp	Gly	Val	Gly	Leu	Cys	Phe	Thr	Leu	Asn	Leu	Ala	
185			35					40					45				
187	gtg	gct	gat	acc	ttg	att	ggc	gtg	gct	att	tct	ggg	cta	gtt	aca	gac	192
188	Val	Ala	Asp	Thr	Leu	Ile	Gly	Val	Ala	Ile	Ser	Gly	Leu	Val	Thr	Asp	
189			50					55					60				
191	cag	ctc	tcc	agc	tct	gct	cag	cac	aca	cag	aag	acc	ttg	tgt	agc	ctt	240
192	Gln	Leu	Ser	Ser	Ser	Ala	Gln	His	Thr	Gln	Lys	Thr	Leu	Cys	Ser	Leu	
193	65						70						75			80	
195	cgg	atg	gca	ttc	gtc	act	tct	tct	gca	gcc	gcc	tct	gtc	ctc	acg	gtc	288
196	Arg	Met	Ala	Phe	Val	Thr	Ser	Ser	Ala	Ala	Ala	Ser	Val	Leu	Thr	Val	
197						85					90					95	
199	atg	ctg	att	gcc	ttt	gac	agg	tac	ctg	gcc	att	aag	cag	ccc	ctc	cgt	336
200	Met	Leu	Ile	Ala	Phe	Asp	Arg	Tyr	Leu	Ala	Ile	Lys	Gln	Pro	Leu	Arg	
201				100						105					110		
203	tac	ttc	cag	atc	atg	aat	ggg	ctt	gta	gcc	gga	gga	tgc	att	gca	ggg	384
204	Tyr	Phe	Gln	Ile	Met	Asn	Gly	Leu	Val	Ala	Gly	Gly	Cys	Ile	Ala	Gly	
205				115					120						125		
207	ctg	tgg	ttg	ata	tct	tac	ctt	atc	ggc	ttc	ctc	cca	ctt	gga	gtc	tcc	432
208	Leu	Trp	Leu	Ile	Ser	Tyr	Leu	Ile	Gly	Phe	Leu	Pro	Leu	Gly	Val	Ser	
209			130						135				140				
211	ata	ttc	cag	cag	acc	acc	tac	cat	ggg	ccc	tgc	acc	ttc	ttt	gct	gtg	480
212	Ile	Phe	Gln	Gln	Thr	Thr	Tyr	His	Gly	Pro	Cys	Thr	Phe	Phe	Ala	Val	
213	145						150					155				160	
215	ttt	cac	cca	agg	ttt	gtg	ctg	acc	ctc	tcc	tgt	gct	ggc	ttc	ttc	cca	528
216	Phe	His	Pro	Arg	Phe	Val	Leu	Thr	Leu	Ser	Cys	Ala	Gly	Phe	Phe	Pro	
217					165						170					175	
219	gct	gtg	ctc	ctc	ttt	gtc	ttc	ttc	tac	tgt	gac	atg	ctc	aag	att	gcc	576
220	Ala	Val	Leu	Leu	Phe	Val	Phe	Phe	Tyr	Cys	Asp	Met	Leu	Lys	Ile	Ala	
221				180						185					190		
223	tct	gtg	cac	agc	cag	cac	atc	cgg	aag	atg	gaa	cat	gca	gga	gcc	atg	624
224	Ser	Val	His	Ser	Gln	His	Ile	Arg	Lys	Met	Glu	His	Ala	Gly	Ala	Met	
225				195					200					205			
227	gtt	gga	gct	tgc	cgg	ccc	cca	cgg	cct	gtc	aat	gac	ttc	aag	gct	gtc	672
228	Val	Gly	Ala	Cys	Arg	Pro	Pro	Arg	Pro	Val	Asn	Asp	Phe	Lys	Ala	Val	
229			210						215				220				
231	cgg	act	gta	tct	gtc	ctt	att	ggg	agc	ttc	acc	ctg	tcc	tgg	tct	ccg	720
232	Arg	Thr	Val	Ser	Val	Leu	Ile	Gly	Ser	Phe	Thr	Leu	Ser	Trp	Ser	Pro	
233	225					230					235					240	
235	ttt	ctc	atc	act	agc	att	gtg	cag	gtg	gcc	tgc	cac	aaa	tgc	tgc	ctc	768
236	Phe	Leu	Ile	Thr	Ser	Ile	Val	Gln	Val	Ala	Cys	His	Lys	Cys	Cys	Leu	
237					245						250					255	
239	tac	caa	gtg	ctg	gaa	aaa	tac	ctc	tgg	ctc	ctt	gga	gtt	ggc	aac	tcc	816
240	Tyr	Gln	Val	Leu	Glu	Lys	Tyr	Leu	Trp	Leu	Leu	Gly	Val	Gly	Asn	Ser	
241				260						265					270		
243	ctg	ctc	aac	cca	ctc	atc	tat	gcc	tat	tgg	cag	agg	gag	gtt	cgg	cag	864

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244 Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln Arg Glu Val Arg Gln
245          275          280          285
247 cag ctc tgc cac atg gcc ctg ggg gtg aag aag ttc ttt act tca atc 912
248 Gln Leu Cys His Met Ala Leu Gly Val Lys Lys Phe Phe Thr Ser Ile
249      290          295          300
251 ttc ctc ctt ctc tcg gcc agg aat cgt ggt cca cag agg acc cga gaa 960
252 Phe Leu Leu Leu Ser Ala Arg Asn Arg Gly Pro Gln Arg Thr Arg Glu
253 305          310          315          320
255 agc tcc tat cac atc gtc act atc agc cag ccg gag ctc gat ggc tag 1008
256 Ser Ser Tyr His Ile Val Thr Ile Ser Gln Pro Glu Leu Asp Gly
257      325          330          335
260 <210> SEQ ID NO: 4
261 <211> LENGTH: 335
262 <212> TYPE: PRT
263 <213> ORGANISM: Rattus sp.
265 <400> SEQUENCE: 4
266 Met Glu Ser Ser Phe Ser Phe Gly Val Ile Leu Ala Val Leu Thr Ile
267 1          5          10          15
268 Leu Ile Ile Ala Val Asn Ala Leu Val Val Val Ala Met Leu Leu Ser
269      20          25          30
270 Ile Tyr Lys Asn Asp Gly Val Gly Leu Cys Phe Thr Leu Asn Leu Ala
271      35          40          45
272 Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Val Thr Asp
273      50          55          60
274 Gln Leu Ser Ser Ser Ala Gln His Thr Gln Lys Thr Leu Cys Ser Leu
275 65          70          75          80
276 Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ala Ser Val Leu Thr Val
277      85          90          95
278 Met Leu Ile Ala Phe Asp Arg Tyr Leu Ala Ile Lys Gln Pro Leu Arg
279      100          105          110
280 Tyr Phe Gln Ile Met Asn Gly Leu Val Ala Gly Gly Cys Ile Ala Gly
281      115          120          125
282 Leu Trp Leu Ile Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Val Ser
283      130          135          140
284 Ile Phe Gln Gln Thr Thr Tyr His Gly Pro Cys Thr Phe Phe Ala Val
285 145          150          155          160
286 Phe His Pro Arg Phe Val Leu Thr Leu Ser Cys Ala Gly Phe Phe Pro
287      165          170          175
288 Ala Val Leu Leu Phe Val Phe Phe Tyr Cys Asp Met Leu Lys Ile Ala
289      180          185          190
290 Ser Val His Ser Gln His Ile Arg Lys Met Glu His Ala Gly Ala Met
291      195          200          205
292 Val Gly Ala Cys Arg Pro Pro Arg Pro Val Asn Asp Phe Lys Ala Val
293      210          215          220
294 Arg Thr Val Ser Val Leu Ile Gly Ser Phe Thr Leu Ser Trp Ser Pro
295 225          230          235          240
296 Phe Leu Ile Thr Ser Ile Val Gln Val Ala Cys His Lys Cys Cys Leu
297      245          250          255
298 Tyr Gln Val Leu Glu Lys Tyr Leu Trp Leu Leu Gly Val Gly Asn Ser

```

VERIFICATION SUMMARY

DATE: 11/02/2004

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Output Set: N:\CRF4\11022004\J511549.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date